

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=4; day=15; hr=18; min=35; sec=53; ms=492;]

=====

Application No: 10564665 Version No: 2.0

Input Set:

Output Set:

Started: 2008-04-01 10:59:55.302
Finished: 2008-04-01 10:59:57.381
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 79 ms
Total Warnings: 21
Total Errors: 0
No. of SeqIDs Defined: 31
Actual SeqID Count: 31

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)

Input Set:

Output Set:

Started: 2008-04-01 10:59:55.302
Finished: 2008-04-01 10:59:57.381
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 79 ms
Total Warnings: 21
Total Errors: 0
No. of SeqIDs Defined: 31
Actual SeqID Count: 31

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Irie, Reiko
 Tsunoda, Hiroyuki
 Igawa, Tomoyuki
 Sekimori, Yasuo
 Tsuchiya, Masayuki

<120> IgM PRODUCTION BY TRANSFORMED CELL AND
 METHOD OF QUANTIFYING THE SAME

<130> 14875-155US1

<140> 10564665

<141> 2006-09-21

<150> PCT/JP2004/010444

<151> 2004-07-15

<150> US 60/487,333

<151> 2003-07-15

<160> 31

<170> PatentIn version 3.1

<210> 1

<211> 1779

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1779)

<400> 1

atg gag ttt ggg ctg agc tgg ctt ttt ctt gtg gct att tta aaa ggt	48
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly	
1 5 10 15	

gtc cag tgt gag gtg cag ctg ttg gat tct ggg gga ggc ttg gta cag	96
Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln	
20 25 30	

cct ggg ggg tgc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttt	144
Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe	
35 40 45	

agc agc tgt gcc atg agc tgg gtc cgc cag gct cca ggg aag ggg ctg	192
Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu	
50 55 60	

gag tgg gtc tca gct att agt ggt agt ggt ggt agc aca tac tac gca	240
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala	
65 70 75 80	

gac tcc gtg aag ggc cgg ttc acc atc tcc aga gac aaa tcc aag aac	288
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn	
85 90 95	
acg ttg tat ctg caa atg aac agc ctg aga gcc gag gac acg gcc gta	336
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val	
100 105 110	
tat tac tgt gcg aaa ggt ggc aac gat att ttg act ggt tat tat gct	384
Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala	
115 120 125	
tgg ggc cag gga acc ctg gtc acc gtc tcc tca ggg agt gca tcc gcc	432
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala	
130 135 140	
cca acc ctt ttc ccc ctc gtc tcc tgt gag aat tcc ccg tcg gat acg	480
Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr	
145 150 155 160	
agc agc gtg gcc gtt ggc tgc ctc gca cag gac ttc ctt ccc gac tcc	528
Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser	
165 170 175	
atc act ttc tcc tgg aaa tac aag aac aac tct gac atc agc agc acc	576
Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr	
180 185 190	
cgg ggc ttc cca tca gtc ctg aga ggg ggc aag tac gca gcc acc tca	624
Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser	
195 200 205	
cag gtg ctg ctg cct tcc aag gac gtc atg cag ggc aca gac gaa cac	672
Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His	
210 215 220	
gtg gtg tgc aaa gtc cag cac ccc aac ggc aac aaa gaa aag aac gtg	720
Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val	
225 230 235 240	
cct ctt cca gtg att gct gag ctg cct ccc aaa gtg agc gtc ttc gtc	768
Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val	
245 250 255	
cca ccc cgc gac ggc ttc ttc ggc aac ccc cgc aag tcc aag ctc atc	816
Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile	
260 265 270	
tgc cag gcc acg ggt ttc agt ccc cgg cag att cag gtg tcc tgg ctg	864
Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu	
275 280 285	
cgc gag ggg aag cag gtg ggg tct ggc gtc acc acg gac cag gtg cag	912
Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln	
290 295 300	
gct gag gcc aaa gag tct ggg ccc acg acc tac aag gtg acc agc aca	960

Ala	Glu	Ala	Lys	Glu	Ser	Gly	Pro	Thr	Thr	Tyr	Lys	Val	Thr	Ser	Thr		
305					310					315					320		
ctg	acc	atc	aaa	gag	agc	gac	tgg	ctc	ggc	cag	agc	atg	ttc	acc	tgc	1008	
Leu	Thr	Ile	Lys	Glu	Ser	Asp	Trp	Leu	Gly	Gln	Ser	Met	Phe	Thr	Cys		
325					330					335							
cgc	gtg	gat	cac	agg	ggc	ctg	acc	ttc	cag	cag	aat	gcg	tcc	tcc	atg	1056	
Arg	Val	Asp	His	Arg	Gly	Leu	Thr	Phe	Gln	Gln	Asn	Ala	Ser	Ser	Met		
340					345					350							
tgt	gtc	ccc	gat	caa	gac	aca	gcc	atc	cgg	gtc	ttc	gcc	atc	ccc	cca	1104	
Cys	Val	Pro	Asp	Gln	Asp	Thr	Ala	Ile	Arg	Val	Phe	Ala	Ile	Pro	Pro		
355					360					365							
tcc	ttt	gcc	agc	atc	ttc	ctc	acc	aag	tcc	acc	aag	ttg	acc	tgc	ctg	1152	
Ser	Phe	Ala	Ser	Ile	Phe	Leu	Thr	Lys	Ser	Thr	Lys	Leu	Thr	Cys	Leu		
370					375					380							
gtc	aca	gac	ctg	acc	acc	tat	gac	agc	gtg	acc	atc	tcc	tgg	acc	cgc	1200	
Val	Thr	Asp	Leu	Thr	Thr	Tyr	Asp	Ser	Val	Thr	Ile	Ser	Trp	Thr	Arg		
385					390					395					400		
cag	aat	ggc	gaa	gct	gtg	aaa	acc	cac	acc	aac	atc	tcc	gag	agc	cac	1248	
Gln	Asn	Gly	Glu	Ala	Val	Lys	Thr	His	Thr	Asn	Ile	Ser	Glu	Ser	His		
405					410					415							
ccc	aat	gcc	act	ttc	agc	gcc	gtg	ggt	gag	gcc	agc	atc	tgc	gag	gat	1296	
Pro	Asn	Ala	Thr	Phe	Ser	Ala	Val	Gly	Glu	Ala	Ser	Ile	Cys	Glu	Asp		
420					425					430							
gac	tgg	aat	tcc	ggg	gag	agg	ttc	acg	tgc	acc	gtg	acc	cac	aca	gac	1344	
Asp	Trp	Asn	Ser	Gly	Glu	Arg	Phe	Thr	Cys	Thr	Val	Thr	His	Thr	Asp		
435					440					445							
ctg	ccc	tcg	cca	ctg	aag	cag	acc	atc	tcc	cgg	ccc	aag	ggg	gtg	gcc	1392	
Leu	Pro	Ser	Pro	Leu	Lys	Gln	Thr	Ile	Ser	Arg	Pro	Lys	Gly	Val	Ala		
450					455					460							
ctg	cac	agg	ccc	gat	gtc	tac	ttg	ctg	cca	cca	gcc	cgg	gag	cag	ctg	1440	
Leu	His	Arg	Pro	Asp	Val	Tyr	Leu	Leu	Pro	Pro	Ala	Arg	Glu	Gln	Leu		
465					470					475					480		
aac	ctg	cgg	gag	tcg	gcc	acc	atc	acg	tgc	ctg	gtg	acg	ggc	ttc	tct	1488	
Asn	Leu	Arg	Glu	Ser	Ala	Thr	Ile	Thr	Cys	Leu	Val	Thr	Gly	Phe	Ser		
485					490					495							
ccc	gcg	gac	gtc	ttc	gtg	cag	tgg	atg	cag	agg	ggg	cag	ccc	ttg	tcc	1536	
Pro	Ala	Asp	Val	Phe	Val	Gln	Trp	Met	Gln	Arg	Gly	Gln	Pro	Leu	Ser		
500					505					510							
ccg	gag	aag	tat	gtg	acc	agc	gcc	cca	atg	cct	gag	ccc	cag	gcc	cca	1584	
Pro	Glu	Lys	Tyr	Val	Thr	Ser	Ala	Pro	Met	Pro	Glu	Pro	Gln	Ala	Pro		
515					520					525							
ggc	cgg	tac	ttc	gcc	cac	agc	atc	ctg	acc	gtg	tcc	gaa	gag	gaa	tgg	1632	
Gly	Arg	Tyr	Phe	Ala	His	Ser	Ile	Leu	Thr	Val	Ser	Glu	Glu	Glu	Trp		

530	535	540	
aac acg ggg gag acc tac acc tgc gtg gtg gcc cat gag gcc ctg ccc			1680
Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro			
545	550	555	560
aac agg gtc acc gag agg acc gtg gac aag tcc acc ggt aaa ccc acc			1728
Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr			
	565	570	575
ctg tac aac gtg tcc ctg gtc atg tcc gac aca gct ggc acc tgc tac			1776
Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr			
	580	585	590
tga			1779
<210> 2			
<211> 592			
<212> PRT			
<213> Homo sapiens			
<400> 2			
Met Glu Phe Gly Leu Ser Trp Leu Phe Leu Val Ala Ile Leu Lys Gly			
1	5	10	15
Val Gln Cys Glu Val Gln Leu Leu Asp Ser Gly Gly Gly Leu Val Gln			
	20	25	30
Pro Gly Gly Cys Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe			
	35	40	45
Ser Ser Cys Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu			
	50	55	60
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala			
65	70	75	80
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Lys Ser Lys Asn			
	85	90	95
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val			
	100	105	110
Tyr Tyr Cys Ala Lys Gly Gly Asn Asp Ile Leu Thr Gly Tyr Tyr Ala			
	115	120	125
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Ser Ala Ser Ala			
	130	135	140
Pro Thr Leu Phe Pro Leu Val Ser Cys Glu Asn Ser Pro Ser Asp Thr			
145	150	155	160
Ser Ser Val Ala Val Gly Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser			
	165	170	175
Ile Thr Phe Ser Trp Lys Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr			
	180	185	190

Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser		
195	200	205
Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln Gly Thr Asp Glu His		
210	215	220
Val Val Cys Lys Val Gln His Pro Asn Gly Asn Lys Glu Lys Asn Val		
225	230	235 240
Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys Val Ser Val Phe Val		
	245	250 255
Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile		
	260	265 270
Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile Gln Val Ser Trp Leu		
	275	280 285
Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr Thr Asp Gln Val Gln		
290	295	300
Ala Glu Ala Lys Glu Ser Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr		
305	310	315 320
Leu Thr Ile Lys Glu Ser Asp Trp Leu Gly Gln Ser Met Phe Thr Cys		
	325	330 335
Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln Asn Ala Ser Ser Met		
	340	345 350
Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val Phe Ala Ile Pro Pro		
	355	360 365
Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu		
370	375	380
Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg		
385	390	395 400
Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn Ile Ser Glu Ser His		
	405	410 415
Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala Ser Ile Cys Glu Asp		
	420	425 430
Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr Val Thr His Thr Asp		
	435	440 445
Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg Pro Lys Gly Val Ala		
450	455	460
Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu		
465	470	475 480
Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu Val Thr Gly Phe Ser		
	485	490 495

Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg Gly Gln Pro Leu Ser
500 505 510

Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro Glu Pro Gln Ala Pro
515 520 525

Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val Ser Glu Glu Glu Trp
530 535 540

Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala His Glu Ala Leu Pro
545 550 555 560

Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser Thr Gly Lys Pro Thr
565 570 575

Leu Tyr Asn Val Ser Leu Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
580 585 590

<210> 3
<211> 723
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(723)

<400> 3
atg gtg ttg cag acc cag gtc ttc att tct ctg ttg ctc tgg atc tct 48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
1 5 10 15

ggt gcc tac ggg gac atc gtg atg acc cag tct cca gac tcc ctg gct 96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala
20 25 30

gtg tct ctg ggc gag agg gcc acc atc aac tgc aag tcc agc cag agt 144
Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser
35 40 45

gtt tta tac agc tcc aac aat aag aac tac tta gct tgg tac cag cag 192
Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
50 55 60

aaa cca gga cag cct cct aag ctg ctc att tac tgg gca tct acc cgg 240
Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80

gaa tcc ggg gtc cct gac cga ttc agt ggc agc ggg tct ggg aca gat 288
Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
85 90 95

ttc act ctc acc atc agc agc ctg cag gct gaa gat gtg gca gtt tat 336
Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr
100 105 110

tac tgt cag caa tat tat agt act cct ccg acg ttc ggc caa ggg acc	384
Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr	
115 120 125	
aag gtg gaa atc aaa cga act gtg gct gca cca tct gtc ttc atc ttc	432
Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe	
130 135 140	
ccg cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc	480
Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys	
145 150 155 160	
ctg ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg	528
Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val	
165 170 175	
gat aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag	576
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln	
180 185 190	
gac agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc	624
Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser	
195 200 205	
aaa gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat	672
Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His	
210 215 220	
cag ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt	720
Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
225 230 235 240	
tag	723
<210> 4	
<211> 240	
<212> PRT	
<213> Homo sapiens	
<400> 4	
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser	
1 5 10 15	
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala	
20 25 30	
Val Ser Leu Gly Glu Arg Ala	